

IN THE SPECIFICATION

Please amend the specification as follows:

Please replace the two paragraphs beginning at page 11, lines 26-29 with the following:

Figure 5 shows the alignment of *Brassica* consensus centromere satellite repeats, BB5R4-1 (SEQ ID NO:2), BB5R4-1 (SEQ ID NO:51), and BB280R2-3 (SEQ ID NO:52).

Figure 6 shows the alignment of *Glycine max* (soybean) consensus centromere satellite repeats, CrGM1 (SEQ ID NO:25), CrGm2 (SEQ ID NO:26), and SB12MC (SEQ ID NO:24).

Please replace the paragraph starting at page 22, line 3 with the following:

The comparison of sequences and determination of percent identity between two nucleotide sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (1970) J. Mol. Biol. 48:444-453 algorithm which has been incorporated into the GAP program in the GCG software package (~~available at www.gcg.com~~), using either a Blossum 62 matrix or a PAM250 matrix. Preferably parameters are set so as to maximize the percent identity.

Please replace Table 1 starting at page 31, line 16 with the following:

Table 1: *Bacillus thurinsiensis* Endotoxin Genes^a

New Nomenclature	Old Nomenclature	GenBank Accession
Cry1Aa	Cry1A(a)	M11250
Cry1Ab	Cry1A(b)	M13898
Cry1Ac	Cry1A(c)	M11068
Cry1Ad	Cry1A(d)	M73250
Cry1Ae	Cry1A(e)	M65252

Cry1Ba	Cry1B	X06711
Cry1Bb	ET5	L32020
Cry1Bc	PEG5	Z46442
Cry1Bd	CryEI	U70726
Cry1Ca	Cry1C	X07518
Cry1Cb	Cry1C(b)	M97880
Cry 1 Da	Cry1D	X54160
Cry1Db	PrtB	Z22511
Cry1Ea	Cry1E	X53985
Cry1Eb	Cry1E(b)	M73253
Cry 1 Fa	Cry1F	M63897
Cry1Fb	PrtD	Z22512
Cry1Ga	PrtA	Z22510
Cry 1Gb	CryH2	U70725
Cry 1 Ha	PrtC	Z22513
Cry1Hb		U35780
Cry 1 Ia	CryV	X62821
Cry lib	CryV	U07642
Cry1Ja	ET4	L32019
Cry1Jb	ET1	U31527
Cry1K		U28801
Cry2Aa	Cry1IA	M31738
Cry2Ab	Cry1IB	M23724
Cry2Ac	Cry1IC	X57252
Cry3A	Cry1IIA	M22472
Cry3Ba	Cry1IIB	X17123
Cry3Bb	CryIIIB2	M89794
Cry3C	Cry1IID	X59797

Cry4A	Cry1VA	Y00423
Cry4B	Cry1VB	X07423
Cry5Aa	CryVA(a)	L07025
Cry5Ab	CryVA(b)	L07026
Cry6A	Cry VIA	L07022
Cry6B	CryVIB	L07024
Cry7Aa	Cry1IIC	M64478
Cry7Ab	Cry1IICb	U04367
Cry8A	Cry1IIE	U04364
Cry8B	Cry1IIG	U04365
Cry8C	Cry1IIF	U04366
Cry9A	Cry1G	X58120
Cry9B	Cry IX	X75019
Cry9C	Cry1H	Z37527
Cry10A	Cry1VC	M12662
Cry1IA	Cry1VD	M31737
Cry1IB	Jeg80	X86902
Cry12A	CryVB	L07027
Cry13A	CryVC	L07023
Cry14A	CryVD	U13955
Cry15A	34kDa	M76442
Cry16A	cbm71	X94146
Cry17A	cbm71	X99478
Cry18A	CryBPI	X99049
Cry19A	Jeg65	Y08920
CytIAa	CytA	X03182
CytIAb	CytM	X98793
Cyt2A	CytB	Z14147

Cyt2B	CytB	U52043
^a Adapted from: http://epunix.biol.susx.ac.uk/Home/Neil_Crickmore/Bt/index.html Crickmore, N, Zeigler, DR, Feitelson, J. et al. 1998. Revision of the Nomenclature for the <i>Bacillus thuringiensis</i> Pesticidal Crystal Proteins. <i>Microbiol. Molec. Biol. Rev.</i> 62:807-813.		

Please replace Table 2, beginning at page 63, line 16, with the following:

Table 2: *Drosophila melanogaster* Promoters ~~(Information obtained from the Flybase Web Site at <http://flybase.bio.indiana.edu/> which is a database of the *Drosophila* Genome)~~
(adapted from the *Drosophila* FlyBase, referenced in Grumblin, G. and Strelets, V. FlyBase: anatomical data, images and queries. *Nucl. Acids Rsrch.* 34:D484-8.

Seq Id No.	Symbol	Flybase ID	Standard promoter gene name	Gene Product	Chromosome
4	gd	FBgn0004654	Phosphogluconate dehydrogenase	6-phosphogluconate dehydrogenase	X
5	rim	FBgn0015946	grim	grim-P138	3
5	ro	FBgn0003961	Urate oxidase	Uro-P1	2
7	na	FBgn0003448	snail	sna-P1	2
8	h3	FBgn0003249	Rhodopsin 3	Rh3	3
9	sp-1 γ	FBgn0002564	Larval serum protein 1 γ	Lsp1γ-P1	3

***Saccharomyces cerevisiae* Promoters**

~~(Information obtained from the *Saccharomyces* Genome Database Web site at <http://www.yeastgenome.org/SearchContents.shtml>~~
(adapted from information available from the *Saccharomyces* Genome Database, referenced in Dwight SS, Balakrishnan R, Christie KR, et al. 2004. *Saccharomyces* genome database: underlying principles and organisation. *Brief Bioinform.* 5:9-22).

Seq Id No.	Symbol	Systematic Name	Standard promoter gene name	Gene Product	Chromosome
10	ef-2	YBR118W	TEF2 (Translation elongation factor promoter <u>promoter</u>)	Translation elongation factor EF-1 alpha	2
11	eu-1	YGL009C	LEU1 (LEUcine biosynthesis)	isopropylmalate isomerase	7
12	et16	YPR167C	METHionine requiring	3 'phosphoadenyly lsulfate reductase	16
13	eu-2	YCL018W	LEU2 (leucine biosynthesis)	beta-IPM (isopropylmalate) dehydrogenase	3
14	is-4	YCL030C	HIS4 (HISTidine requiring)	histidinol dehydrogenase	3
15	et-2	YNL277W	MET2 (methionine requiring)	L-homoserine-O- acetyltransferase	14
16	te-3	YKL178C	STE3 (alias DAF2 Sterile)	a-factor receptor	11
17	rg-1	YOL058W	ARG1 (alias ARG10 ARGinine requiring)	arginosuccinate synthetase	15
18	gk-1	YCR012W	PGK1 (phosphoglycerate kinase)	phosphoglycerate kinase	3
19	PD-1	YDL022W	GPD1 (alias DAR1/HOR1/OSG1/OSR5: glycerol-3-phosphate dehydrogenase activity	glycerol-3- phosphate dehydrogenase	4
20	DH1	YOL086C	ADH1 (alias ADC1)	alcohol dehydrogenase	15
21	PD-2	YOL059W	GPD2 (alias GPD3: glycerol-	glycerol-3-	15

			3-phosphate dehydrogenase activity	phosphate dehydrogenase	
22	rg-4	YHR018C	ARGinine requiring	argininosuccinate lyase	8
23	at-1	YAR035W	YAT-1 (carnitine acetyltransferase)	carnitine acetyltransferase	1